

SEQUENCE LISTING

<110> Serrero, Ginette

<120> 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

<130> Z9996.488/P001-A

<140> 08/991,862

<141> 1997-12-16

<150> 08/863,862

<151> 1997-05-23

<160> 17

<170> PatentIn Ver. 2.0

<210> 1

<211> 2137

<212> DNA

<213> Mouse epithelin/granulin

<220>

<221> CDS

<222> (23)..(1789)

<223> The sequence is identical to that of the published mouse granulin except for one nucleotide (T instead of G) at position 1071 of GP88 cDNA (position 1056 of mouse granulin).

<400> 1

```

cggacccccga cgcagacaga cc atg tgg gtc ctg atg agc tgg ctg gcc ttc 52
                        Met Trp Val Leu Met Ser Trp Leu Ala Phe
                          1                      5                      10

gcg gca ggg ctg gta gcc gga aca cag tgt cca gat ggg cag ttc tgc 100
Ala Ala Gly Leu Val Ala Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys
                      15                      20                      25

cct gtt gcc tgc tgc ctt gac cag gga gga gcc aac tac agc tgc tgt 148
Pro Val Ala Cys Cys Leu Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys
                      30                      35                      40

aac cct ctt ctg gac aca tgg cct aga ata acg agc cat cat cta gat 196
Asn Pro Leu Leu Asp Thr Trp Pro Arg Ile Thr Ser His His Leu Asp
                      45                      50                      55

ggc tcc tgc cag acc cat ggc cac tgt cct gct ggc tat tct tgt ctt 244
Gly Ser Cys Gln Thr His Gly His Cys Pro Ala Gly Tyr Ser Cys Leu
                      60                      65                      70

ctc act gtg tct ggg act tcc agc tgc tgc ccg ttc tct aag ggt gtg 292
Leu Thr Val Ser Gly Thr Ser Ser Cys Cys Pro Phe Ser Lys Gly Val
                      75                      80                      85

tct tgt ggt gat ggc tac cac tgc tgc ccc cag ggc ttc cac tgt agt 340
Ser Cys Gly Asp Gly Tyr His Cys Cys Pro Gln Gly Phe His Cys Ser
                      95                      100                      105

```

gca gat ggg aaa tcc tgc ttc cag atg tca gat aac ccc ttc ggt gct	388
Ala Asp Gly Lys Ser Cys Phe Gln Met Ser Asp Asn Pro Leu Gly Ala	
110 115 120	
gtc cag tgt cct ggg agc cag ttt gaa tgt cct gac tct gcc acc tgc	436
Val Gln Cys Pro Gly Ser Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys	
125 130 135	
tgc att atg gtt gat ggt tcg tgg gga tgt tgt ccc atg ccc cag gcc	484
Cys Ile Met Val Asp Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala	
140 145 150	
tct tgc tgt gaa gac aga gtg cat tgc tgt ccc cat ggg gcc tcc tgt	532
Ser Cys Cys Glu Asp Arg Val His Cys Cys Pro His Gly Ala Ser Cys	
155 160 165 170	
gac ctg gtt cac aca cga tgc gtt tca ccc acg ggc acc cac acc cta	580
Asp Leu Val His Thr Arg Cys Val Ser Pro Thr Gly Thr His Thr Leu	
175 180 185	
cta aag aag ttc cct gca caa aag acc aac agc gca gtg tct ttg cct	628
Leu Lys Lys Phe Pro Ala Gln Lys Thr Asn Ser Ala Val Ser Leu Pro	
190 195 200	
ttt tct gtc gtg tgc cct gat gct aag acc cag tgt ccc gat gat tct	676
Phe Ser Val Val Cys Pro Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser	
205 210 215	
acc tgc tgt gag cta ccc act ggg aag tat ggc tgc tgt cca atg ccc	724
Thr Cys Cys Glu Leu Pro Thr Gly Lys Tyr Gly Cys Cys Pro Met Pro	
220 225 230	
aat gcc atc tgc tgt tcc gac cac ctg cac tgc tgc ccc cag gac act	772
Asn Ala Ile Cys Cys Ser Asp His Leu His Cys Cys Pro Gln Asp Thr	
235 240 245 250	
gta tgt gac ctg atc cag agt aag tgc cta tcc aag aac tac acc acg	820
Val Cys Asp Leu Ile Gln Ser Lys Cys Leu Ser Lys Asn Tyr Thr Thr	
255 260 265	
gat ctc ctg acc aag ctg cct gga tac cca gtg aag gag gtg aag tgc	868
Asp Leu Leu Thr Lys Leu Pro Gly Tyr Pro Val Lys Glu Val Lys Cys	
270 275 280	
gac atg gag gtg agc tgc cct gaa gga tat acc tgc tgc cgc ctc aac	916
Asp Met Glu Val Ser Cys Pro Glu Gly Tyr Thr Cys Cys Arg Leu Asn	
285 290 295	
act ggg gcc tgg ggc tgc tgt cca ttt gcc aag gcc gtg tgt tgt gac	964
Thr Gly Ala Trp Gly Cys Cys Pro Phe Ala Lys Ala Val Cys Cys Asp	
300 305 310	
gat cac att cat tgc tgc ccg gca ggg ttt cag tgt cac aca gag aaa	1012
Asp His Ile His Cys Cys Pro Ala Gly Phe Gln Cys His Thr Glu Lys	
315 320 325 330	
gga acc tgc gaa atg ggt atc ctc caa gta ggg tgg atg aag aag gtc	1060
Gly Thr Cys Glu Met Gly Ile Leu Gln Val Gly Trp Met Lys Lys Val	
335 340 345	

ata gcc ccc ctc cgc ctg cca gac cca cag atc ttg aag agt gat aca	1108
Ile Ala Pro Leu Arg Leu Pro Asp Pro Gln Ile Leu Lys Ser Asp Thr	
350 355 360	
cct tgt gat gac ttc act agg tgt cct aca aac aat acc tgc tgc aaa	1156
Pro Cys Asp Asp Phe Thr Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys	
365 370 375	
ctc aat tct ggg gac tgg ggc tgc tgt ccc atc cca gag gct gtc tgc	1204
Leu Asn Ser Gly Asp Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys	
380 385 390	
tgc tca gac aac cag cat tgc tgc cct cag ggc ttc aca tgt ctg gct	1252
Cys Ser Asp Asn Gln His Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala	
395 400 405 410	
cag ggg tac tgt cag aag gga gac aca atg gtg gct ggc ctg gag aag	1300
Gln Gly Tyr Cys Gln Lys Gly Asp Thr Met Val Ala Gly Leu Glu Lys	
415 420 425	
ata cct gcc cgc cag aca acc ccg ctc caa att gga gat atc ggt tgt	1348
Ile Pro Ala Arg Gln Thr Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys	
430 435 440	
gac cag cat acc agc tgc cca gta ggg caa acc tgc tgc cca agc ctc	1396
Asp Gln His Thr Ser Cys Pro Val Gly Gln Thr Cys Cys Pro Ser Leu	
445 450 455	
aag gga agt tgg gcc tgc tgc cag ctg ccc cat gct gtg tgc tgt gag	1444
Lys Gly Ser Trp Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu	
460 465 470	
gac cgg cag cac tgt tgc ccg gcc ggg tac acc tgc aac gtg aag gcg	1492
Asp Arg Gln His Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala	
475 480 485 490	
agg acc tgt gag aag gat gtc gat ttt atc cag cct ccc gtg ctc ctg	1540
Arg Thr Cys Glu Lys Asp Val Asp Phe Ile Gln Pro Pro Val Leu Leu	
495 500 505	
acc ctc ggc cct aag gtt ggg aat gtg gag tgt gga gaa ggg cat ttc	1588
Thr Leu Gly Pro Lys Val Gly Asn Val Glu Cys Gly Glu Gly His Phe	
510 515 520	
tgc cat gat aac cag acc tgt tgt aaa gac agt gca gga gtc tgg gcc	1636
Cys His Asp Asn Gln Thr Cys Cys Lys Asp Ser Ala Gly Val Trp Ala	
525 530 535	
tgc tgt ccc tac cta aag ggt gtc tgc tgt aga gat gga cgt cac tgt	1684
Cys Cys Pro Tyr Leu Lys Gly Val Cys Cys Arg Asp Gly Arg His Cys	
540 545 550	
tgc ccc ggt ggc ttc cac tgt tca gcc agg gga acc aag tgt ttg cga	1732
Cys Pro Gly Gly Phe His Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg	
555 560 565 570	
aag aag att cct cgc tgg gac atg ttt ttg agg gat ccg gtc cca aga	1780
Lys Lys Ile Pro Arg Trp Asp Met Phe Leu Arg Asp Pro Val Pro Arg	
575 580 585	

ccg cta ctg taaggaaggg ctacagactt aaggaactcc acagtcctgg 1829
 Pro Leu Leu

gaaccctgtt ccgagggtac ccactactca ggcctcccta gcgcctcctc ccctaacgtc 1889
 tccccggcct actcactctg agtcacccta tcaccatggg aggtggagcc tcaaactaaa 1949
 accttctttt atggaaagaa ggctctggcc aaaagccccg tatcaaactg ccatttcttc 2009
 cggtttctgt ggaccttggt gccaggtgct cttcccgagc cacaggtgtt ctgtgagctt 2069
 gcttgtgtgt gtgtgcgcgt gtgcgtgtgt tgctccaata aagtttgtac gctttctgaa 2129
 aaaaaaaaaa 2137

<210> 2
 <211> 589
 <212> PRT
 <213> Mouse epithelin/granulin

<400> 2
 Met Trp Val Leu Met Ser Trp Leu Ala Phe Ala Ala Gly Leu Val Ala
 1 5 10 15
 Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
 20 25 30
 Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys Asn Pro Leu Leu Asp Thr
 35 40 45
 Trp Pro Arg Ile Thr Ser His His Leu Asp Gly Ser Cys Gln Thr His
 50 55 60
 Gly His Cys Pro Ala Gly Tyr Ser Cys Leu Leu Thr Val Ser Gly Thr
 65 70 75 80
 Ser Ser Cys Cys Pro Phe Ser Lys Gly Val Ser Cys Gly Asp Gly Tyr
 85 90 95
 His Cys Cys Pro Gln Gly Phe His Cys Ser Ala Asp Gly Lys Ser Cys
 100 105 110
 Phe Gln Met Ser Asp Asn Pro Leu Gly Ala Val Gln Cys Pro Gly Ser
 115 120 125
 Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys Cys Ile Met Val Asp Gly
 130 135 140
 Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg
 145 150 155 160
 Val His Cys Cys Pro His Gly Ala Ser Cys Asp Leu Val His Thr Arg
 165 170 175
 Cys Val Ser Pro Thr Gly Thr His Thr Leu Leu Lys Lys Phe Pro Ala
 180 185 190
 Gln Lys Thr Asn Ser Ala Val Ser Leu Pro Phe Ser Val Val Cys Pro
 195 200 205

Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser Thr Cys Cys Glu Leu Pro
 210 215 220
 Thr Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Ile Cys Cys Ser
 225 230 235 240
 Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile Gln
 245 250 255
 Ser Lys Cys Leu Ser Lys Asn Tyr Thr Thr Asp Leu Leu Thr Lys Leu
 260 265 270
 Pro Gly Tyr Pro Val Lys Glu Val Lys Cys Asp Met Glu Val Ser Cys
 275 280 285
 Pro Glu Gly Tyr Thr Cys Cys Arg Leu Asn Thr Gly Ala Trp Gly Cys
 290 295 300
 Cys Pro Phe Ala Lys Ala Val Cys Cys Asp Asp His Ile His Cys Cys
 305 310 315 320
 Pro Ala Gly Phe Gln Cys His Thr Glu Lys Gly Thr Cys Glu Met Gly
 325 330 335
 Ile Leu Gln Val Gly Trp Met Lys Lys Val Ile Ala Pro Leu Arg Leu
 340 345 350
 Pro Asp Pro Gln Ile Leu Lys Ser Asp Thr Pro Cys Asp Asp Phe Thr
 355 360 365
 Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys Leu Asn Ser Gly Asp Trp
 370 375 380
 Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp Asn Gln His
 385 390 395 400
 Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala Gln Gly Tyr Cys Gln Lys
 405 410 415
 Gly Asp Thr Met Val Ala Gly Leu Glu Lys Ile Pro Ala Arg Gln Thr
 420 425 430
 Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys Asp Gln His Thr Ser Cys
 435 440 445
 Pro Val Gly Gln Thr Cys Cys Pro Ser Leu Lys Gly Ser Trp Ala Cys
 450 455 460
 Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His Cys Cys
 465 470 475 480
 Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Thr Cys Glu Lys Asp
 485 490 495
 Val Asp Phe Ile Gln Pro Pro Val Leu Leu Thr Leu Gly Pro Lys Val
 500 505 510
 Gly Asn Val Glu Cys Gly Glu Gly His Phe Cys His Asp Asn Gln Thr
 515 520 525

Cys Cys Lys Asp Ser Ala Gly Val Trp Ala Cys Cys Pro Tyr Leu Lys
 530 535 540
 Gly Val Cys Cys Arg Asp Gly Arg His Cys Cys Pro Gly Gly Phe His
 545 550 555 560
 Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg Lys Lys Ile Pro Arg Trp
 565 570 575
 Asp Met Phe Leu Arg Asp Pro Val Pro Arg Pro Leu Leu
 580 585

<210> 3
 <211> 19
 <212> PRT
 <213> mouse granulin

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Internal peptide of mouse GP88 used to raise the
 antisera against the GP88 used in the
 immunoaffinity step.

<400> 3
 Lys Lys Val Ile Ala Pro Arg Arg Leu Pro Asp Pro Gln Ile Leu Lys
 1 5 10 15

Ser Asp Thr

<210> 4
 <211> 12
 <212> PRT
 <213> mouse granulin

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Internal peptide of mouse GP88 used to raise the
 antisera against the GP88 used in the
 immunoaffinity step.

<400> 4
 Pro Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser Thr
 1 5 10

<210> 5
 <211> 14
 <212> PRT
 <213> mouse granulin

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Internal peptide of mouse GP88 used to raise the
 antisera against the GP88 used in the
 immunoaffinity step.

<400> 5

Ser Ala Arg Gly Thr Lys Cys Leu Arg Lys Lys Ile Pro Arg
1 5 10

<210> 6

<211> 19

<212> PRT

<213> Human granulin

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Internal peptide of human GP88 used to develop
neutralizing anti-human GP88 monoclonal antibody.

<400> 6

Glu Lys Ala Pro Ala His Leu Ser Leu Pro Asp Pro Gln Ala Leu Lys
1 5 10 15

Arg Asp Val

<210> 7

<211> 14

<212> PRT

<213> Human granulin

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Internal peptide of human GP88 used to develop
neutralizing anti-human GP88 monoclonal antibody.

<400> 7

Ala Arg Arg Gly Thr Lys Cys Leu Arg Arg Glu Ala Pro Arg
1 5 10

<210> 8

<211> 24

<212> DNA

<213> mammalian

<220>

<221> primer

<222> (1)..(24)

<223> Internal peptide of CMV promoter used as PCR
primer.

<400> 8

cctacttggc agtacatcta cgta

24

<210> 9

<211> 27

<212> DNA

<213> mammalian

<220>
 <221> primer
 <222> (1)..(27)
 <223> GP88 cDNA start codon used as oligonucleotide PCR primer.

 <400> 9
 cgagaattca ggcagaccat gtgggtc 27

 <210> 10
 <211> 27
 <212> DNA
 <213> mammalian

 <220>
 <221> primer
 <222> (1)..(27)
 <223> Antisense primer oligonucleotide primer

 <400> 10
 cgagaattca ggcagaccat gtgggtc 27

 <210> 11
 <211> 23
 <212> DNA
 <213> mammalian

 <220>
 <221> primer
 <222> (1)..(23)
 <223> Antisense primer oligonucleotide primer

 <400> 11
 ctgacggttc actaaacgag ctc 23

 <210> 12
 <211> 25
 <212> DNA
 <213> mammalian

 <220>
 <221> primer
 <222> (1)..(25)
 <223> primer

 <400> 12
 ggatccacgg agttgttacc tgatc 25

 <210> 13
 <211> 25
 <212> DNA
 <213> mammalian

 <220>
 <221> primer
 <222> (1)..(25)
 <223> oligonucleotide PCR primer

<400> 13
gaattcgcag gcagaccatg tggac 25

<210> 14
<211> 21
<212> DNA
<213> mammalian

<220>
<221> primer
<222> (1)..(21)
<223> Antisense oligonucleotide to human GP88

<400> 14
gggtccacat ggtctgcctg c 21

<210> 15
<211> 24
<212> DNA
<213> mammalian

<220>
<221> primer
<222> (1)..(24)
<223> Antisense oligonucleotide to human GP88

<400> 15
gccaccagcc ctgctgttaa ggcc 24

<210> 16
<211> 2095
<212> DNA
<213> Human GP88 cDNA

<220>
<221> CDS
<222> (13)..(1791)
<223> Nucleotide sequence of human granulin/epithelin precursor (human GP88). Human Granulin Genebank M75161.

<400> 16
cgcaggcaga cc atg tgg acc ctg gtg agc tgg gtg gcc tta aca gca ggg 51
Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly
1 5 10

ctg gtg gct gga acg cgg tgc cca gat ggt cag ttc tgc cct gtg gcc 99
Leu Val Ala Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala
15 20 25

tgc tgc ctg gac ccc gga gga gcc agc tac agc tgc tgc cgt ccc ctt 147
Cys Cys Leu Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu
30 35 40 45

ctg gac aaa tgg ccc aca aca ctg agc agg cat ctg ggt ggc ccc tgc 195
Leu Asp Lys Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys
50 55 60

cag gtt gat gcc cac tgc tct gcc ggc cac tcc tgc atc ttt acc gtc Gln Val Asp Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val	243
65 70 75	
tca ggg act tcc agt tgc tgc ccc ttc cca gag gcc gtg gca tgc ggg Ser Gly Thr Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly	291
80 85 90	
gat ggc cat cac tgc tgc cca cgg ggc ttc cac tgc agt gca gac ggg Asp Gly His His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly	339
95 100 105	
cga tcc tgc ttc caa aga tca ggt aac aac tcc gtg ggt gcc atc cag Arg Ser Cys Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln	387
110 115 120 125	
tgc cct gat agt cag ttc gaa tgc ccg gac ttc tcc acg tgc tgt gtt Cys Pro Asp Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val	435
130 135 140	
atg gtc gat ggc tcc tgg ggg tgc tgc ccc atg ccc cag gct tcc tgc Met Val Asp Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys	483
145 150 155	
tgt gaa gac agg gtg cac tgc tgt ccg cac ggt gcc ttc tgc gac ctg Cys Glu Asp Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu	531
160 165 170	
gtt cac acc cgc tgc atc aca ccc acg ggc acc cac ccc ctg gca aag Val His Thr Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys	579
175 180 185	
aag ctc cct gcc cag agg act aac agg gca gtg gcc ttg tcc agc tcg Lys Leu Pro Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser	627
190 195 200 205	
gtc atg tgt ccg gac gca cgg tcc cgg tgc cct gat ggt tct acc tgc Val Met Cys Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys	675
210 215 220	
tgt gag ctg ccc agt ggg aag tat ggc tgc tgc cca atg ccc aac gcc Cys Glu Leu Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala	723
225 230 235	
acc tgc tgc tcc gat cac ctg cac tgc tgc ccc caa gac act gtg tgt Thr Cys Cys Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys	771
240 245 250	
gac ctg atc cag agt aag tgc ctc tcc aag gag aac gct acc acg gac Asp Leu Ile Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp	819
255 260 265	
ctc ctc act aag ctg cct gcg cac aca gtg ggc gat gtg aaa tgt gac Leu Leu Thr Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp	867
270 275 280 285	
atg gag gtg agc tgc cca gat ggc tat acc tgc tgc cgt cta cag tcg Met Glu Val Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser	915
290 295 300	

ggg gcc tgg ggc tgc tgc cct ttt acc cag gct gtg tgc cgt gag gac Gly Ala Trp Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp 305 310 315	963
cac ata cac tgc tgt ccc gcg ggg ttt acg tgt gac acg cag aag ggt His Ile His Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly 320 325 330	1011
acc tgt gaa cag ggg ccc cac cag gtg ccc tgg atg gag aag gcc cca Thr Cys Glu Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro 335 340 345	1059
gct cac ctc agc ctg cca gac cca caa gcc ttg aag aga gat gtc ccc Ala His Leu Ser Leu Ser Asp Pro Gln Ala Leu Lys Arg Asp Val Pro 350 355 360 365	1107
tgt gat aat gtc agc agc tgt ccc tcc tcc gat acc tgc tgc caa ctc Cys Asp Asn Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu 370 375 380	1155
acg tct ggg gag tgg ggc tgc tgt cca atc cca gag gct gtc tgc tgc Thr Ser Gly Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys 385 390 395	1203
tcg gac cac cag cac tgc tgc ccc cag cga tac acg tgt gta gct gag Ser Asp His Gln His Cys Cys Pro Gln Arg Tyr Thr Cys Val Ala Glu 400 405 410	1251
ggg cag tgt cag cga gga agc gag atc gtg gct gga ctg gag aag atg Gly Gln Cys Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met 415 420 425	1299
cct gcc cgc cgc ggt tcc tta tcc cac ccc aga gac atc ggc tgt gac Pro Ala Arg Arg Gly Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp 430 435 440 445	1347
cag cac acc agc tgc ccg gtg ggc gga acc tgc tgc ccg agc cag ggt Gln His Thr Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Gln Gly 450 455 460	1395
ggg agc tgg gcc tgc tgc cag ttg ccc cat gct gtg tgc tgc gag gat Gly Ser Trp Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp 465 470 475	1443
cgc cag cac tgc tgc ccg gct ggc tac acc tgc aac gtg aag gct cga Arg Gln His Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg 480 485 490	1491
tcc tgc gag aag gaa gtg gtc tct gcc cag cct gcc acc ttc ctg gcc Ser Cys Glu Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala 495 500 505	1539
cgt agc cct cac gtg ggt gtg aag gac gtg gag tgt ggg gaa gga cac Arg Ser Pro His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His 510 515 520 525	1587
ttc tgc cat gat aac cag acc tgc tgc cga gac aac cga cag ggc tgg Phe Cys His Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp 530 535 540	1635

gcc tgc tgt ccc tac gcc cag ggc gtc tgt tgt gct gat cgg cgc cac 1683
 Ala Cys Cys Pro Tyr Ala Gln Gly Val Cys Cys Ala Asp Arg Arg His
 545 550 555

 tgc tgt cct gct ggc ttc cgc tgc gca cgc agg ggt acc aag tgt ttg 1731
 Cys Cys Pro Ala Gly Phe Arg Cys Ala Arg Arg Gly Thr Lys Cys Leu
 560 565 570

 cgc agg gag gcc ccg cgc tgg gac gcc cct ttg agg gac cca gcc ttg 1779
 Arg Arg Glu Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu
 575 580 585

 aga cag ctg ctg tgagggacag tactgaagac tctgcagccc tcgggacccc 1831
 Arg Gln Leu Leu
 590

 actcggaggg tgccctctgc tcaggcctcc ctagcacctc cccctaacca aattctccct 1891
 ggacccatt ctgagctccc catcaccatg ggaggtgggg cctcaatcta aggccttcc 1951
 ctgtcagaag ggggttgagg caaaagccca ttacaagctg ccatccctc cccgtttcag 2011
 tggaccctgt gccaggtgc tttccctat ccacaggggt gtttgtgtgt tgggtgtgct 2071
 ttcaataaag tttgtcactt tctt 2095

<210> 17
 <211> 593
 <212> PRT
 <213> Human GP88 cDNA

<400> 17
 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala
 1 5 10 15

 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
 20 25 30

 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys
 35 40 45

 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp
 50 55 60

 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr
 65 70 75 80

 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His
 85 90 95

 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys
 100 105 110

 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp
 115 120 125

 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp
 130 135 140

Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp
 145 150 155 160
 Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr
 165 170 175
 Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro
 180 185 190
 Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys
 195 200 205
 Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu
 210 215 220
 Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys
 225 230 235 240
 Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile
 245 250 255
 Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr
 260 265 270
 Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val
 275 280 285
 Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp
 290 295 300
 Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His
 305 310 315 320
 Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu
 325 330 335
 Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu
 340 345 350
 Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn
 355 360 365
 Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly
 370 375 380
 Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His
 385 390 395 400
 Gln His Cys Cys Pro Gln Arg Tyr Thr Cys Val Ala Glu Gly Gln Cys
 405 410 415
 Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg
 420 425 430
 Arg Gly Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr
 435 440 445
 Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Gln Gly Gly Ser Trp
 450 455 460

Ala	Cys	Cys	Gln	Leu	Pro	His	Ala	Val	Cys	Cys	Glu	Asp	Arg	Gln	His
465					470					475					480
Cys	Cys	Pro	Ala	Gly	Tyr	Thr	Cys	Asn	Val	Lys	Ala	Arg	Ser	Cys	Glu
				485					490					495	
Lys	Glu	Val	Val	Ser	Ala	Gln	Pro	Ala	Thr	Phe	Leu	Ala	Arg	Ser	Pro
			500					505					510		
His	Val	Gly	Val	Lys	Asp	Val	Glu	Cys	Gly	Glu	Gly	His	Phe	Cys	His
		515					520					525			
Asp	Asn	Gln	Thr	Cys	Cys	Arg	Asp	Asn	Arg	Gln	Gly	Trp	Ala	Cys	Cys
	530					535					540				
Pro	Tyr	Ala	Gln	Gly	Val	Cys	Cys	Ala	Asp	Arg	Arg	His	Cys	Cys	Pro
545					550					555					560
Ala	Gly	Phe	Arg	Cys	Ala	Arg	Arg	Gly	Thr	Lys	Cys	Leu	Arg	Arg	Glu
				565					570						575
Ala	Pro	Arg	Trp	Asp	Ala	Pro	Leu	Arg	Asp	Pro	Ala	Leu	Arg	Gln	Leu
			580					585					590		
Leu															